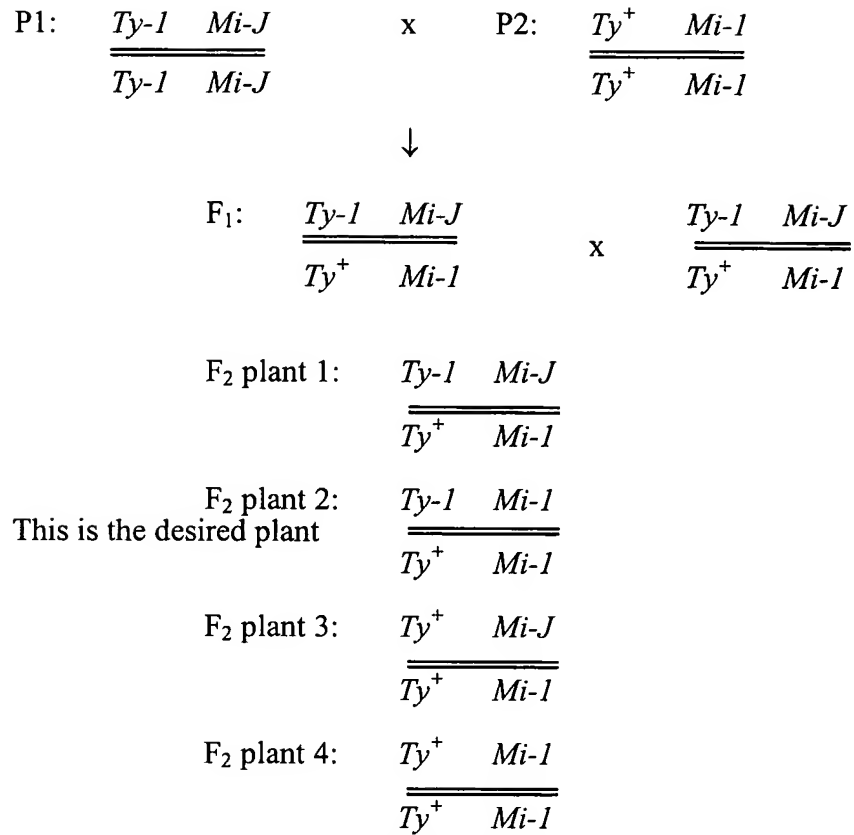


FIGURE 1



as well as other genotypes would be produced in the F2. By selfing plant number 2 completely homozygous plants for *Ty-l* and *Mi-l* can be identified.

FIGURE 2



Ty-1 assay

A = resistant allele, 303 & 95
bp

B = susceptible allele, 398 bp

FIGURE 3

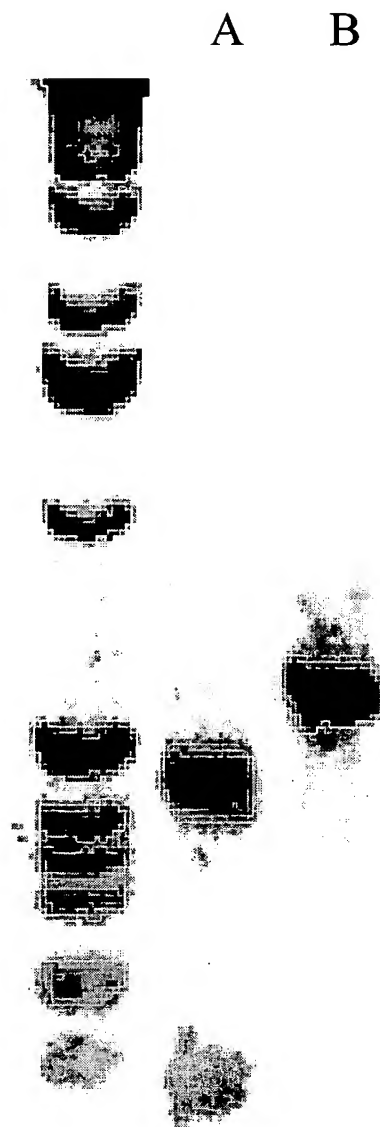


FIGURE 4

A B

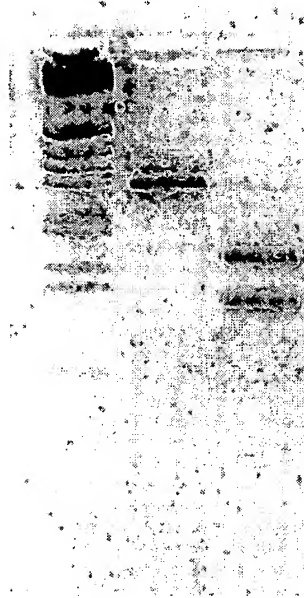


FIGURE 5

Ty-/- SEQ ID NO.: 10

Ty+/- SEQ ID NO.: 11

SEQ ID NO:1

5' T A A T C C G T C G T T A C C T C T C C T T

1 C T A A T C C G T C G T T A C C T C T C C T T T G A A C T A A A A T T T T T T T G T C A A A A G T Ty-/-
1 C T A A T C C G T C G T T A C C T C T C C T T T G A A C T A A A A T T T T T T T G T C A A A A G T Ty+/-

51 A C A A A T C T G T T T A T T T T A T A T T T T T T T T T C T T G G A A T T T A C T A T C G A T T A Ty-/-
51 A C A A A T C T G T T T A T T T T A T A T T T T T T T T C T T G G A A T T T A C T A T C T T T A Ty+/-

101 T T T T G T A A T T A G A A G G T T A G A A T T G G A G T A T A T G T T G T G A T T G G A A C Ty-/-
100 T T T T G T A A T T A G A A G G T T A G A A T T G G A G T A T A T G T T G T G A T T G G A A C Ty+/-

151 A T T T G T T G T T G C C T T T A T G G T G G C A A T T A T G T T T A C A T G T G T C A T T G G C Ty-/-
150 A T T T G T T T T G C C T T T A T G G T G G C A A T T A T G T T T A C A T G T G T C A T T G G C Ty+/-

201 A A C T T A C T G A G T C A T C T T T A C T T T T T A A T A A G A A T G C T T T C A A A T G T T T A Ty-/-
200 A A C T T A C T G A G T C A T C T T T T T A A T A A G A A T G C T T T C A A A T G T T T A Ty+/-

251 A A T T T C A T T A G C T C A A T G G T A A T T G T A T T T A T T G A T G C A T A T A T C T T T Ty-/-
250 A A T T T C A T T A G C T C A A T G G T A A T T G T A T T T A T T G A T G C A T A T A T C T T T Ty+/-

301 T G T T C T A G T T T C T G A T T A T A T C A T G T A N C G A A A C T T A T A T A A A A A T A A Ty-/-
300 T G T T C T A G T T T C T G A T T A T A T C A T G T A C G A A A C T T A T A T A A A A A A T A A Ty+/-

351 T A G T A A T A G T A G T A G A A N A T T T A T G A C A T C A T T G C T A T T G A A G T C A T C C Ty-/-
350 T A G T A A T A G T A G T A G A A N A T T T A T G A C A T C A T T G C T A T T G A A G T C A T C C Ty+/-

AGT AACGATAACTTCAGTAGGC

401 G A A T C T

399 G A A T C T A M C

SEQ ID NO:2

FIGURE 6

Mi+ - SEQ ID NO.: 7
 Mi-1 - SEQ ID NO.: 8
 Mi-J - SEQ ID NO.: 9

```

1  GACACGGACCCACTATTCTGAAACTGATGGTCATTCTCTCTCTTATCGGAGCCTTGCTGATCTTCCAGCTCTTGCAGCAAAATGACTAGCTTGAC  Mi+.seq
1  GACACGGACCCACTATTCTGAAACGATGGTCATTCTCTCTCTTATCGGAGCCTTGCTGATCTTCCGCTCTTGCAGCAAAATGACTAGCTTGAC  Mi-1.seq
1  GACACGGACCCACTATTCTGAAACTGATGGTCATTCTCTCTCTTATCGGAGCCTTGCTGATCTTCCAGCTCTTGCAGCAAAATGACTAGCTTGAC  Mi-J.seq

101 GTAAGGGATCTGCACCTACATCGGTATCCTGTTGAGTTGCATAACCCAGAAACCTGGACCTTGCTTTGACTTTTTTACCTGATTCACGATGACACCTTT  Mi+.seq
101 GTAAGGGATCTGCACCTACATCGGTATCCTGTTGAGTTGCATAACCCAGAAACCTGGACCTTGCTTTGACTTTTTTACCTGATTCACGATGACACCTTT  Mi-1.seq
101 GTAAGGGATCTGCACCTACATCGGTATCCTGTTGAGTTGCATAACCCAGAAACCTGGACCTTGCTTTGACTTTTTTACCTGATTCACGATGACACCTTT  Mi-J.seq

201 CTCTCTAATTCAGCTTCAGATAATAGATCATAACTCTTGCCATTGCAGGCATTATCCCTCTTAACCATACTGGATTATTGGAGAACACATCATTTTCA  Mi+.seq
201 CTCTCTAATTCAGCTTCAGATAATAGATCATAACTCTTGCCATTGCAGGCATTATCCCTCTTAACCATACTGGATTATTGGAGAACACATCATTTTCA  Mi-1.seq
201 CTCTCTAATTCAGCTTCAGATAATAGATCATAACTCTTGCCATTGCAGGCATTATCCCTCTTAACCATACTGGATTATTGGAGAACACATCATTTTCA  Mi-J.seq

301 CCATCAGAAGACCTCTTTGGGACTACAAGTGGGTAAAGCTGAAGAGGGAGCAACAGAGGTCGGGAATTGCATAGATCCCTTTGTGAAGAAATCTGCAGCTT  Mi+.seq
301 CCATCAGAAGACCTCTTTGGGACTACAAGTGGGTAAAGCTGAAGAGGGAGCAACAGAGGTCGGGAATTGCATAGATCCCTTTGTGAAGAAATCTGCAGCTT  Mi-1.seq
301 CCATCAGAAGACCTCTTTGGGACTACAAGTGGGTAAAGCTGAAGAGGGAGCAACAGAGGTCGGGAATTGCATAGATCCCTTTGTGAAGAAATCTGCAGCTT  Mi-J.seq

401 TABACTCAACAAAGATAGAGTACTATCCAGATCTTGCCAGCCTGCTCTCTTTTAACTTGACCTGTTCCAGCACTACCTTTGCTTGCACCTAGTGTCT  Mi+.seq
401 TABACTCAACAAAGATAGAGTACTATCCAGATCTTGCCAGCCTGCTCTCTTTTAACTTGACCTGTTCCAGCACTACCTTTGCTTGCACCTAGTGTCT  Mi-1.seq
401 TABACTCAACAAAGATAGAGTACTATCCAGATCTTGCCAGCCTGCTCTCTTTTAACTTGACCTGTTCCAGCACTACCTTTGCTTGCACCTAGTGTCT  Mi-J.seq

501 CTTCGGGTGAGACAGGAGACCCCTTGCTACCTTTTCTCTCTGAGATGTATCATACATATTTTTCCATAGAACTCTGGGGATTACATGTCAAGGAATCT  Mi+.seq
501 CTTCGGGTGAGACAGGAGACCCCTTGCTACCTTTTCTCTCTGAGATGTATCATACATATTTTTCCATAGAACTCTGGGGATTACATGTCAAGGAATCT  Mi-1.seq
501 CTTCGGGTGAGACAGGAGACCCCTTGCTACCTTTTCTCTCTGAGATGTATCATACATATTTTTCCATAGAACTCTGGGGATTACATGTCAAGGAATCT  Mi-J.seq

601 CGAGTTCTCTCCCTTTCTTAAATCGGAGAAATCATTATTGTACACTTCCCTTATGCGTTGACACATCGGAATATAGCTTCTGGGTTCTTTGCTG  Mi+.seq
601 CGAGTTCTCTCCCTTTCTTAAATCGGAGAAATCATTATTGTACACTTCCCTTATGCGTTGACACATCGGAATATAGCTTCTGGGTTCTTTGCTG  Mi-1.seq
601 CGAGTTCTCTCCCTTTCTTAAATCGGAGAAATCATTATTGTACACTTCCCTTATGCGTTGACACATCGGAATATAGCTTCTGGGTTCTTTGCTG  Mi-J.seq

701 AAACCAAGTCTTTCTTTGAATCATCTCTGAGTCCCTGTTCTTACATTTGTCAGGAATCATCTCTGGCATTTTACTGCTTGAACCTCCATCTAGACTTTTC  Mi+.seq
701 AAACCAAGTCTTTCTTTGAATCATCTCTGAGTCCCTGTTCTTACATTTGTCAGGAATCATCTCTGGCATTTTACTGCTTGAACCTCCATCTAGACTTTTC  Mi-1.seq
701 AAACCAAGTCTTTCTTTGAATCATCTCTGAGTCCCTGTTCTTACATTTGTCAGGAATCATCTCTGGCATTTTACTGCTTGAACCTCCATCTAGACTTTTC  Mi-J.seq

801 AACACACAGGGCCAAAGGCTCTGGTTCTGTCATCGAGTGCATCATCTTATAAATTTTTTGGAGATACATCTGATCCACCTCATTGTTCTTCTCTA  Mi+.seq
801 AACACACAGGGCCAAAGGCTCTGGTTCTGTCATCGAGTGCATCATCTTATAAATTTTTTGGAGATACATCTGATCCACCTCATTGTTCTTCTCTA  Mi-1.seq
801 AACACACAGGGCCAAAGGCTCTGGTTCTGTCATCGAGTGCATCATCTTATAAATTTTTTGGAGATACATCTGATCCACCTCATTGTTCTTCTCTA  Mi-J.seq

901 TTTCATCTCTCCCTAG  Mi+.seq
901 TTTCATCTCTCCCTAG  Mi-1.seq
901 TTTCATCTCTCCCTAG  Mi-J.seq

```

Decoration 'Decoration #1': Shade (with solid deep red) residues that differ from Mi+.seq.
 Decoration 'Decoration #2': Shade (with solid bright cobalt) residues that differ from Mi-J.seq.

FIGURE 7

Mi+ (SEQ ID. NO. 7)

GACACGGACCCACTATTCTGAAACTGATGGTCATTCTTTCTCTCCTTATCGGAGCCTTGGTCTGAGTTTCCAGTCTTGCA
AGCAAAGTGACTAGCTTGACGTAAGGGATCTGCACCTTACATCGGTATCCTGTTGAGTTGCATAACCAGAAACCATGGACT
TTGCTTTGACTTTTTTACCTGATTACGATGAACATCTTTCTCCTCTAATTCAGCTTCAGATAATAGATCATAACTCTTG
CCATTGCAGGCATTATCTTCTTAACCATACTGGATTATTGGAGAACACATCATTTTACCATCAGAAGACCTCTTGGG
ACTAGAAGTGGGTAAGGCTGAAGAGGGAGCAACAGAAGGTCGCGAATTGCATAGATCCTTTTGTGAAGAATCTGCAGCTT
TAACACTCAACAAAGATAGAGTACTATCCAGATCTTGCCAGCCTGCTGTTCCCTTTTAACTTGACCTGTTCCAGCACTA
CCTTTGCTTGCACCTAGTGTCTTCCGGTCAGACAAGGAGACCCTTGCTACCTTTTCCCTTCTAGAGATGTCATCACATAT
TTTTTCCATAGAATCCTGGGATTACATGTCAAGGAATCTCGCAGTTCTCTCCCTTTTCTCTTAATCGGAGAATCATTAT
TGTCACACTTCCCTTATGCGTTGACACATCGGAAATATAAGCTTCTGGGTTCTTTGCTGAAACCAAGTCTTTCTTGAA
TCATCCTCTGAGTCCCTGTTCTTACATTTGTACGAATCATCTCTGGCATTCTTACTGCTTGAACCTCCATCTAGACTTTTC
AACAACAGGGCAAAAGGTCGGTTCTCGTCATCGAGTGCAATCTTGTATAATTTTTTGGGAAGATACATCTGATTCCA
CTTCACTTGTGTTCCCTTCTATTTCATCCTCCGTAG

Mi-1 (SEQ ID. NO. 8)

GACACGGACCCACTATTCTGAAACCGATGGTCATTCTTTCTCTCCTTATCGGAGCCTTGGTCTGAATTTCCCGTCTTGCA
AGCAAATTGACTAGCTTGACGTAAGGGATCTGCACCTTGCATCGGTATCCTGTTGAGTTGCATAACCAGAAACCGTGGACT
TTGCTTTGACTTTTTTACCTGATTACGATGGACATCTTTCTCCTCTAATTCAGCTTCAGATAATAGATCATAACTCTTG
CCATTGCAGGCATTATCTTCTTAACCATACTGGATTATTGGAGAACCACATCATTTTACCATCAGAAGACCTCTTGGC
ACTAGAAGTGGGAAGGCTGAAGAGGGAGCAACAGAAGGTCGCGAATTGCATAGATCCTTTTGTGAAGAATCTGCAGCTT
TAACACTCAACAAAGATAGAGTACTATCCAGATCTTGCCAGCCTGCTGTTCCCTTTTAACTTGACCTGTTCCAGCACTA
CCTTTGCTTGCACCTAGTGTCTTCCGGTCAGACAAGGAGACCCTTGCTACCTTTTCCCTTCTGGAGATGTCATCACATAT
TTTTTCCATAGAATCCTGGGATTACATGTCAAGGAATCTCGAAGTTCTCTCCCTTTTCTCTTAATCGGAGAATCATTAT
TGTCACACTTCCCTTATGCGTTGACACATCGGAAATATAAGCTTCTGGGTTCTTTGCTGAAACCAAGTCTTTCTTGAA
TCATCCTCTGAGTCCCTGTTCTTACATTTCTCAGGAATCATCTCTGGCATTCTTACTGCTTGAACCTCCATCTAGACTTTTC
AACAACAGGGCAGAAGGTCGGTTCTCGTCATCGAGTGCAATCTTGTATAATTTTTTGGGAAGATACATCTGATTCCA
CCTCACTTGTGTTCCCTTCTATTTCATCCTCCGTAG

Mi-J (SEQ ID. NO. 9)

GACACGGACCCACTATTCTGAAACTGATGGTCATTCTTTCTCTCCTTATCGGAGCCTTGGTCTGACTTTCCAGTCTTGCA
AGCAAATTGACTAGCTTGACGTAAGGGATCTGCACCTTACATCGGTATCCTGTTGAGTTGCATAACCAGAAACCGTGGACT
TTGCTTTGACTTTTTTACCTGATTACGATGGACAACCTTTCTCCTCTAATTCAGCTTCAGATAATAGATCATAACTCTTG
CCATTGCAGGCATTATCTTCTTAACCATACTGGATTATTGGAGAACCACATCATTTTACCATCAGAAGACCTCTTGGG
ACTAGAAGTGGGTAAGGCTGAAGAGGGAGCAACAGAAGGTCGCGAATTGCATAGATCCTTTTGTGAAGAATCTGCAGCTT
TAACACTCAACAAAGATAGAGTACTATCCAGATCTTGCCAGCCTGCTGTTCCCTTTTAACTTGACCTGTTCCAGCACTA
CCTTTGCTTGCACCTAGTGTCTTCCGGTCAGACAAGGAGACCCTTGCTACCTTTTCCCTTCTGGAGATGTCATCACATAT
TTTTTCCATAGAATCCTGGGATTACATGTCAAGGAATCTCGAAGTTCTCTCCCTTTTCTCTTAATCGGAGAATCATTAT
TGTCACACTTCCCTTATGCGTTGACACATCGGAAATATAAGCTTCTGGGTTCTTTGCTGAAACCAAGTCTTTCTTGAA
TCATCCTCTGAGTCCCTGTTCTTACATTTGTATGAATCATCTCTGGCATCTTACTGCTTGAACCTCCATCTAGACTTTTC
AACAACAGGGCAGAAGGTCGGTTCTCGTCATCGAGTGCAATCTTGTATAATTTTTTGGGAAGATACATCTGATTCCA
CCTCACTTGTGTTCCCTTCTATTTCATCCTCCGTAG

Ty-1 (SEQ ID. NO. 10)

CTAATCCGTCGTTACCTCTCCTTTGAACTAAAAATTTTTTGTCAAAGTTACAAATCTGTTTATTTTATATATTTTTTTT
CTTGGAATTACTATCGATATTTTTGTAATTAGAAGGTTAGAATTGGAGTATATATGTTGTGATTGGAACGATTGTTGTT
GCCTTTATGGTGGCAATTATGTTTACATGTGTCAATGGCTAACTTACTGAGTCATCTTACTTTTTTAATAAGAATGCTTC
AAATGTTTATAATTTTCACTAGCTCAATGGTAATTGTATTTATTGATGCATATATCTTTTTTGTCTAGTTTCTGATTATA
TCATGTANCGAACTTATATAAAAAATAATTAGTAATAGTAGTAGAANATTTATGACATCATTGCTATTGAAGTCATCCG
GAATCT

Ty + (SEQ ID. NO. 11)

CTAATCCGTCGTTACCTCTCCTTTGAACTAAAAATTTGTGTCAAAGTTACAAATCTGTTTATTTTATATACTTTTTTC
TTGGAATTACTATCTTTATTTTTGTAATTAGAAGGTTAGAATTGGAGTATATATGTTGTGATTGGAACGAGTTGCTATTG
CCTTTATGGTGGAAATTATGTTTACATGTGTCAATGGGTAACCTTACTGAGTCATCTTACTTTTTTAATAAGAATGCTTCA
TATGTTTATAATTTCACTAGCTCAATGGTTATTGTATTTATTGATGCATATATCTTTTTTGTCTAGTTTCTGATTATAT
CATGTAGCGAACTTATATAAAAAATAATTAGTAATAGTAGTAGAATTTATGACATCATTGCTATTGAAGTCATCCGGA
ATCTANCT

Figure 8 - Normalized Pathology Scoring

